



1/5

SEQUENCE LISTING

<110> Croce, Carlo M.
Calin, George A.

<120> NOVEL TUMOR SUPPRESSOR GENE AND
COMPOSITIONS AND METHODS FOR MAKING AND USING THE SAME

<130> 3589.1015-008

<140> 10/530,792

<141> 2003-10-10

<150> PCT/US2003/032270

<151> 2003-10-10

<150> 60/417,842

<151> 2002-10-11

<160> 14

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 3791

<212> DNA

<213> Homo sapiens

<400> 1

```
cacccaagtc tgagttgcta aaaaatggag ctgtcactgg gccttgctct gccaggacct 60
gcagagccgg ggacctctct gtggcaagcc cagcaagatg actgctctga ggcgccctag 120
ggctgagggg ggggccgtga caccagcccc gccccccagc cacctgggaa aaggaagcac 180
aaaaaggaga agcagcaacg gctgctctgc ttcttccca tctcgtcttt ggggtcatgcc 240
tgccagcagc aaagcagctc cataggggag gagagccacg caggatctca cagctgcagt 300
ctaatagtaa cacagaggat tcagcagtgg ccaccatggg ttctgtgaat tccagaggtc 360
acaaggcgga agcccagggt gtgatgatgg gcttgactc ggcgggcaag accacgctcc 420
tttacaagct gaagggccac cagctgggtg agacctgcc cactgttggt ttcaacgtgg 480
agcctctgaa agctcctggg cagctgtcac tgactctctg ggacgttggt gggcaggccc 540
cgctcagagc cagctggaag gactatctgg aaggcacaga tatcctctg tacgtgctgg 600
acagcacaga tgaagccgcg ttacccgagt cggcggtgta gctcacagaa gtcctgaacg 660
accccaacat ggctggcgct cccttcttgg tgctggccaa caagcaggag gcacctgatg 720
cacttccgct gcttaagatc agaaacaggc tgagtctaga gagattccag gaccactgct 780
gggagctccg gggctgcagt gccctcactg gggagggggt gcccgaggcc ctgcagagcc 840
tgtggagcct cctgaaatct cgcagctgca tgtgtctgca ggcgagagcc catggggctg 900
agcgcggaga cagcaagaga tcttgatcca gacagagcag catatctttg ctcatacaaa 960
ctagaagaac cagctgatcc ttgagaaatt tacgcttagt ctatcaaaca agaaatgctg 1020
gcttggcccc gtggctcatg cctgtaatcc cagcactgtg ggagaccacg gtgggggaat 1080
cccttgagcc caggagttag agagcaacat cacaacaccc catttctact aataatcaaa 1140
aaattggccg ggcattggtg catgtgcctg tagtcccagc tacttgggag gctgaggcag 1200
gagaatcgct tgagcccaag aggtagaggt tgcagtgagc caagatcgcg ccactgcact 1260
ccagtctggg caacagagtg agaccctgtc tcaataataa taataataat aatgatgata 1320
ctctaagaaa aaaatctcaa catacttcat ttaatagctc gttaccaagt gtgaatgaag 1380
caatatgtca taatagagta gccactgggt gcataataat agagacctaa attctcaaat 1440
agggaaagag gttttaaaat caaatttgag gccagggtgca gtggctcatg ggcggaggag 1500
ggcagattac ttgaggctag gagttcaaga ccagcctggc caacatggtg aaaccccatc 1560
```

```

tctactgaaa atacaaaaat taggcatagt ggtgcacgcc tgcagtccca gctactcagg 1620
aggttgagggc agaagaatcg cttgaaccca ggaagtggag gttgcagtga gccgagattg 1680
tgctgctgca ctccagcctg ggtgaaaaag acaggctgtg tctccaaaaa gaaaaaaaaa 1740
agtcaaattc aaatatcatc tggacatgtc acaatggatc gcggatcctt atgagtgatt 1800
ttccccagtg gcccctgggg atgtgccact gtcactcaga agggcaagct aggcaggggc 1860
catccaacag caggggtctg caggtttagac gttccctgcc ctgggacgct caccctggg 1920
caagaggctg gaagttcaca ccatccaaaa tttatccttg tttttttct gatgctaatt 1980
agcctctccc gattttatga catcttgtgt tgatctttt caaaaactca ttttctttt 2040
tttctttctc ttttctcctt cttgtagcac atatctttcg ttaaagatca gatcaataaa 2100
atattttatt tattcattaa tttacaaaaa aaaacagagc atttagtttg tggcaaaaac 2160
actgagcttt cgaatatgaa tcatgtgctt taggtgggag ttgtgaattc tgaagataca 2220
gatgacagtg acgaatgcct tctgtctcat gattgacagg gaaaaggaag gttgaccata 2280
gcacccatga aggtcatca ggtgatcatt acctagcatc catgaagcac ctgaaattat 2340
ttgcaaaatg ttacgctttg gaccattttt cgggggaagg agatccagaa ctttttacca 2400
gattttcaaa gacatctgtg actcccaaaa gttaacaatc actgatgtgg ttgttgtatc 2460
cctcatccaa cccagaaca ctttctgtaa tctgagttt ttaatggcaa gtggcctata 2520
tttagcacct gttctcatgt taaacagctc tgaatgttag atattctttc ttatcctgga 2580
ctggttctct ctatctctgg agtaatgcag tataaattgg ccatcagtac cctcctaaaa 2640
tctgagatct gccaggcccc tcttctaaca ccaggttagg catgcttggg tatttccagt 2700
acttgtgagt caacatgttt caagacgctg tgttagacac tagggatgca aagatgaatg 2760
agataaggcc tcaggcctca tgggaaggta gacagtaaag acattactcc cataaaaatg 2820
tgaggagaga gactcagttc agcaactggt tattctgttt attgagcact tacttggacc 2880
aagcactgtg gtcttgggtgt ttacataga ctgtctctaa ttctcacaac tctgcaaaat 2940
atatatattc ccattttata aaactacaaa ctgaggctca gagaagggtg gacctcttgt 3000
tgcttgaggc acagagttat aaagtaacat atctggaatt tgaaatgaga tctgtttagg 3060
gctaattgctg catttttcta caacatcatg cctctagaag gtttaagcta ggtaggcttt 3120
cagccagcag acatgatggg gagagccttc taataagagg gaagagactg cttggaagca 3180
tgaaggagg tgtaagaaag ataagtaagt cagtgtactt gcaacagagg cttgggatga 3240
aggggtgggtg aagttgacat cacgatagaa aacaaaactg gaatgggagt ttaggtccaa 3300
tttgggcaag gttgtttgaa tttcaataat caggggtttg ggtcaaggaa gaaaaatcat 3360
gggacttgcc atttaggagg ataattttgt ggtagtgtgg aggtgaaata aagagaaaag 3420
ggaaccttgg agctgggaag gcaggaaacc ggctagatga ccatcacaca gcaaaggagg 3480
gagtgggaaga gagatgagaa aattgagagc tattattaag aaaaacagtt gagagaggaa 3540
gaatttgaag agggctcaag attttgagtc cacatgacag aaggactgga atgccatgaa 3600
ctggagaagg tgagcgctga agaaccagga tgggacgggg ctggaacagc tgggttcagc 3660
tttgcaggg tgggtacgtg tttggttata gctgctttca gattgttcca ttatctgtac 3720
tccaacaac cctgccggat atatttggtg gctttcactc aaaaaaaaaa aaaaaaaaaa 3780
aaaaaaaaa a 3791

```

<210> 2

<211> 196

<212> PRT

<213> Homo sapiens

<400> 2

```

Met Gly Ser Val Asn Ser Arg Gly His Lys Ala Glu Ala Gln Val Val
 1             5             10             15
Met Met Gly Leu Asp Ser Ala Gly Lys Thr Thr Leu Leu Tyr Lys Leu
 20             25             30
Lys Gly His Gln Leu Val Glu Thr Leu Pro Thr Val Gly Phe Asn Val
 35             40             45
Glu Pro Leu Lys Ala Pro Gly His Val Ser Leu Thr Leu Trp Asp Val
 50             55             60
Gly Gly Gln Ala Pro Leu Arg Ala Ser Trp Lys Asp Tyr Leu Glu Gly
 65             70             75             80
Thr Asp Ile Leu Val Tyr Val Leu Asp Ser Thr Asp Glu Ala Arg Leu
 85             90             95

```

3/5

```

Pro Glu Ser Ala Ala Glu Leu Thr Glu Val Leu Asn Asp Pro Asn Met
      100                      105                      110
Ala Gly Val Pro Phe Leu Val Leu Ala Asn Lys Gln Glu Ala Pro Asp
      115                      120                      125
Ala Leu Pro Leu Leu Lys Ile Arg Asn Arg Leu Ser Leu Glu Arg Phe
      130                      135                      140
Gln Asp His Cys Trp Glu Leu Arg Gly Cys Ser Ala Leu Thr Gly Glu
145                      150                      155                      160
Gly Leu Pro Glu Ala Leu Gln Ser Leu Trp Ser Leu Leu Lys Ser Arg
      165                      170                      175
Ser Cys Met Cys Leu Gln Ala Arg Ala His Gly Ala Glu Arg Gly Asp
      180                      185                      190
Ser Lys Arg Ser
      195

```

<210> 3
 <211> 24
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Ribozyme

<400> 3
 cugaugaguc cgcgaggacg aaac

24

<210> 4
 <211> 26
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Ribozyme

<221> misc_feature
 <222> 1
 <223> n is complementary to the target mRNA flanking the
 5' end of the structural domain

<221> misc_feature
 <222> 26
 <223> n is complementary to the target mRNA flanking the
 3' end of the structural domain.

<400> 4
 ncugaugagu ccgcgaggac gaaacn

26

<210> 5
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer

<400> 5
ccatgggttc tgtgaattcc agagg 25

<210> 6
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 6
cagtggctct ggaatctctc tagac 25

<210> 7
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 7
gccagcagaa agcagctcca tagg 24

<210> 8
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 8
ttcaggaggc tccacaggct ctgc 24

<210> 9
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 9
gaggtatgta ttgaaagaag agg 23

<210> 10
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 10
aacaaaaccc aataacaact cca 23

<210> 11
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 11
cagaagacag tagctgatgt g 21

<210> 12
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 12
gagcaaagat atgctgctct g 21

<210> 13
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 13
gctgagtcca gagagattcc agg 23

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer

<400> 14
tctcgctgc agacacatgc 20